**B**

Competitor	-	DE wt	DE m1	DE m2	DE m3	ARE
Activin injected	- - +	- - +	- - +	- - +	- - +	- - +
Embryo stage	St8 St11					

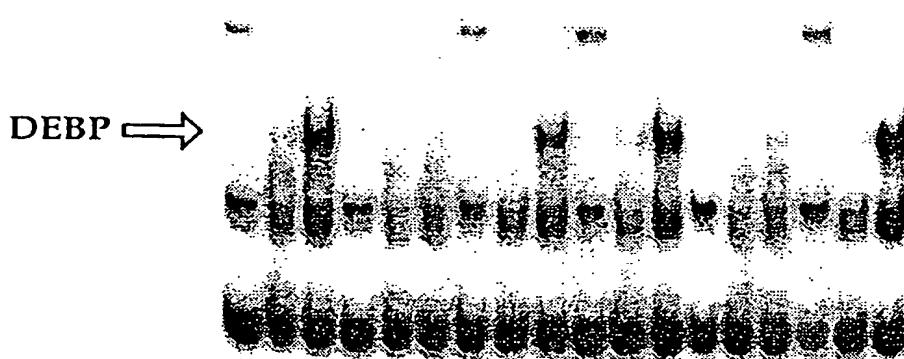


Figure 1

Probe 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

DE wt CATTAATCAGATTAAACGGTGAGCAATTAG

DE m1 --G-C-G--C-G-C-----

DE m2 --G-C-----G-C-----G-C-

DE m3 -----TTGT-----G---

1/30

C

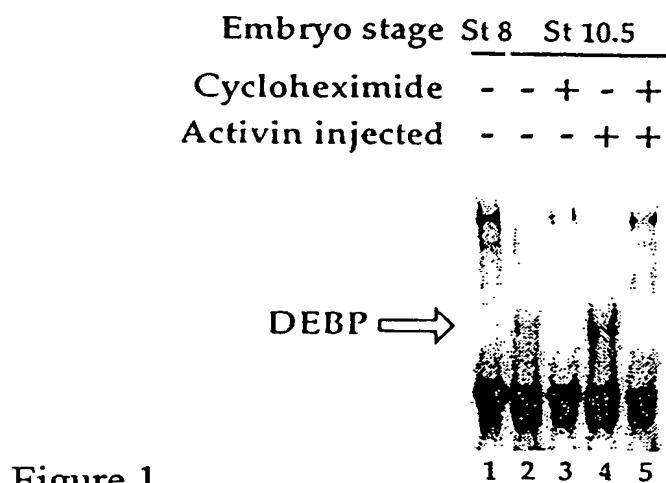
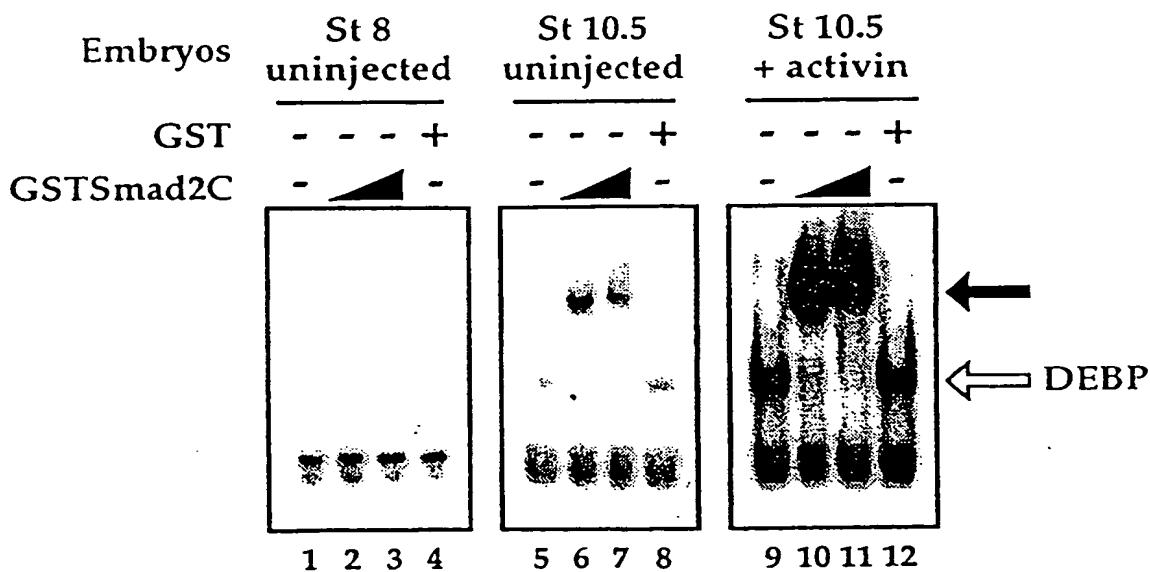
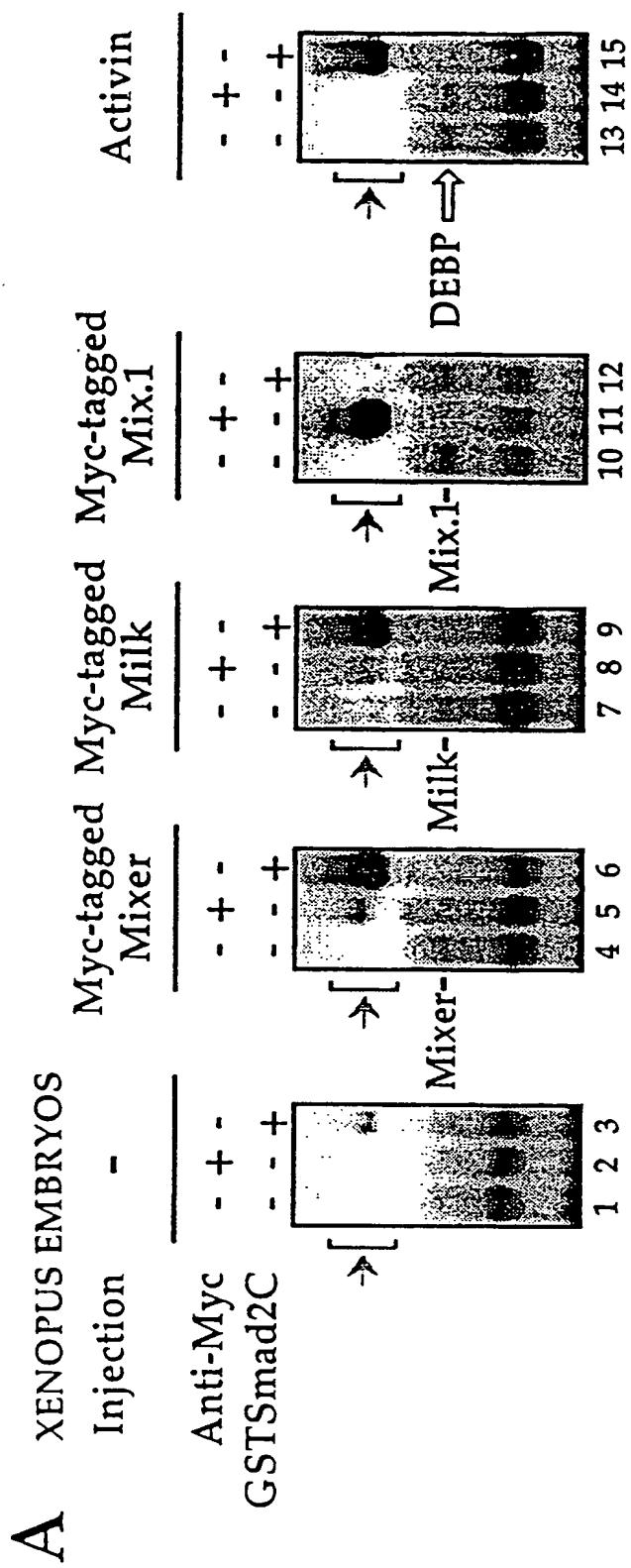


Figure 1

Figure 2





IN VITRO-TRANSLATED

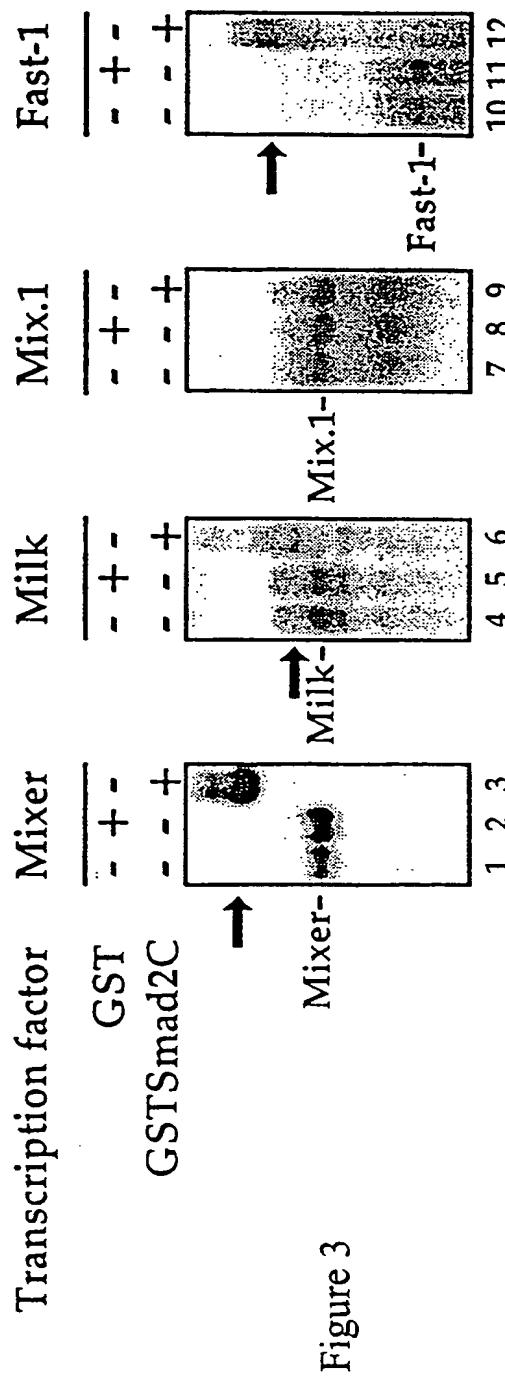


Figure 3

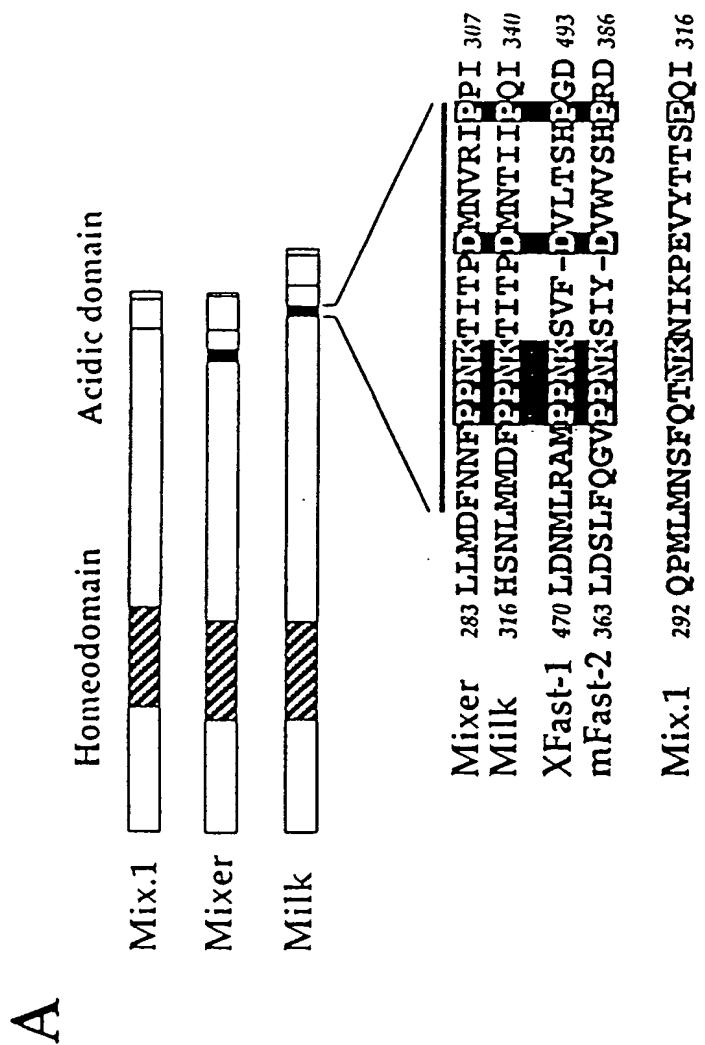


Figure 4

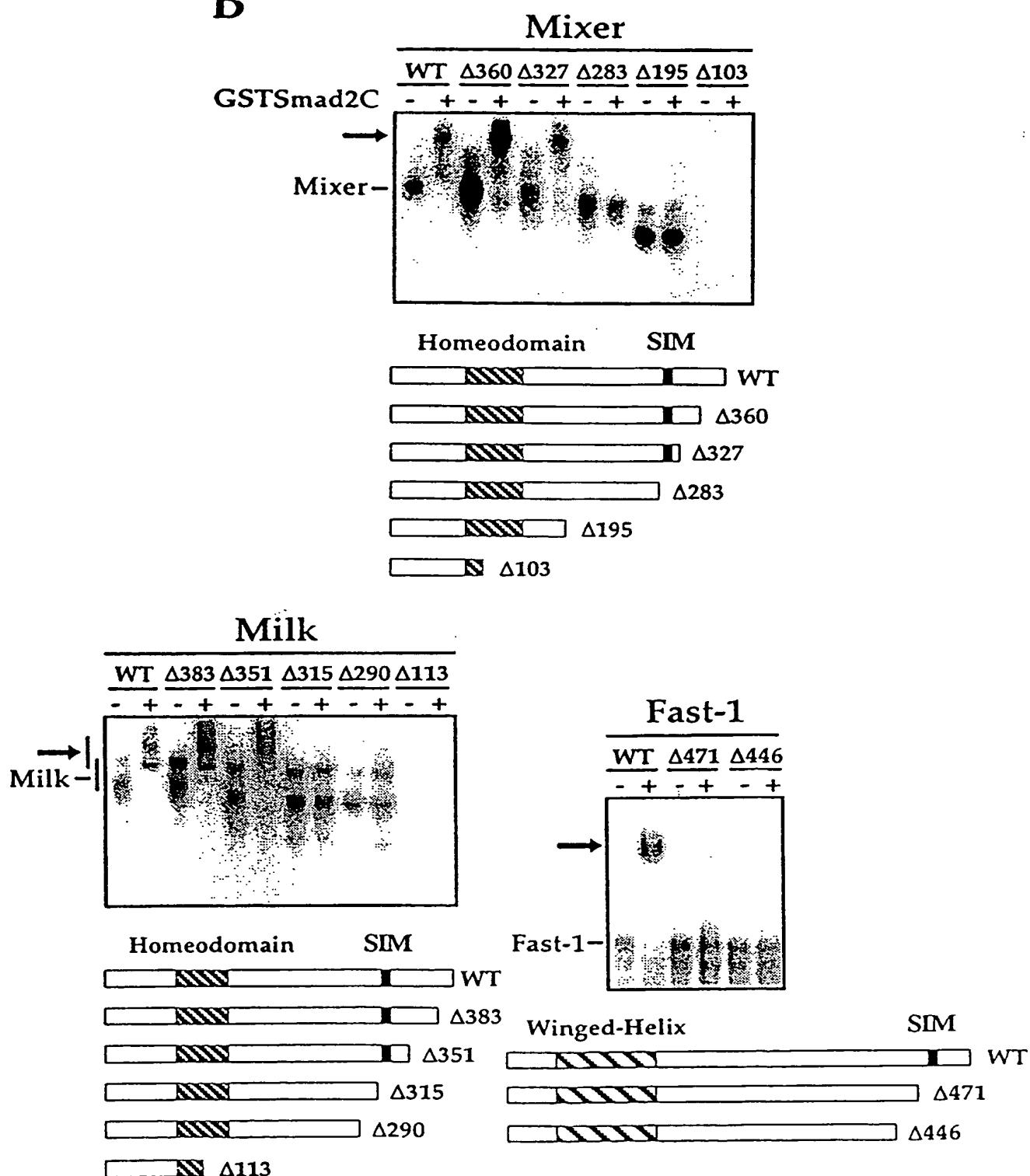
**B**

Figure 4

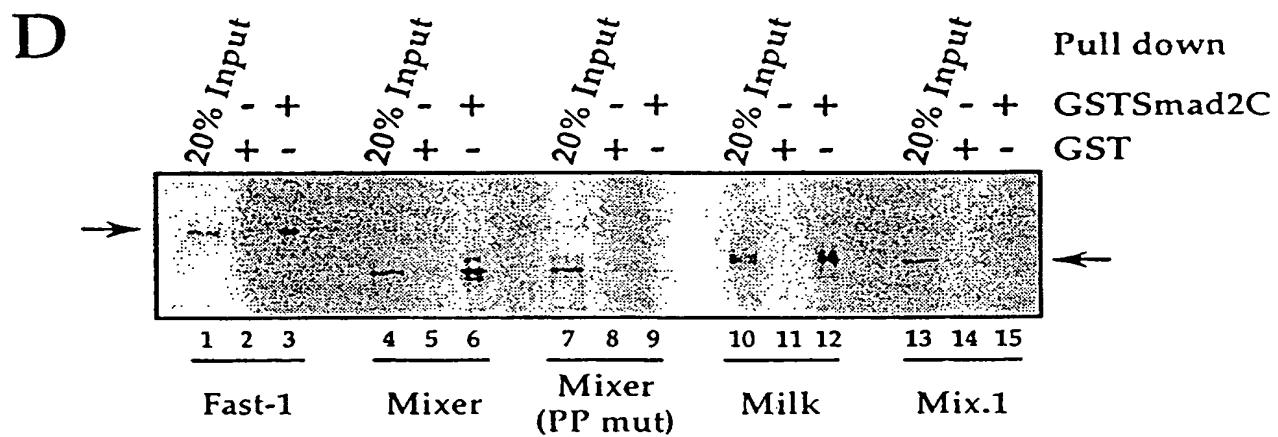
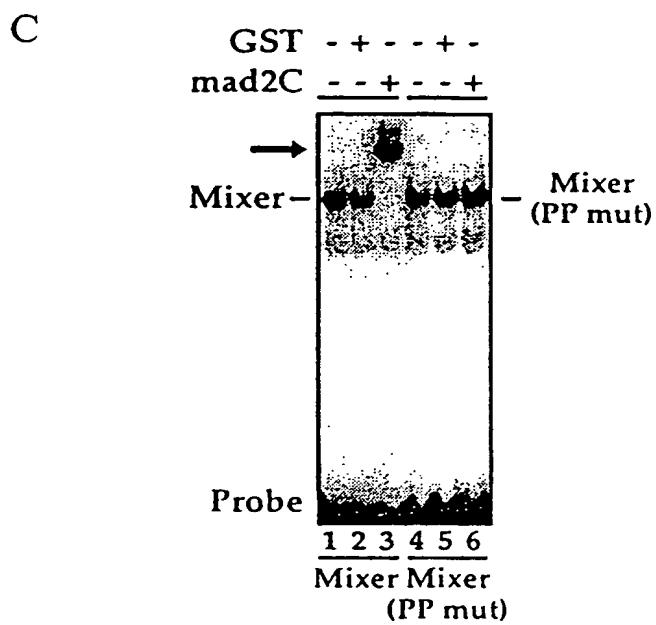


Figure 4

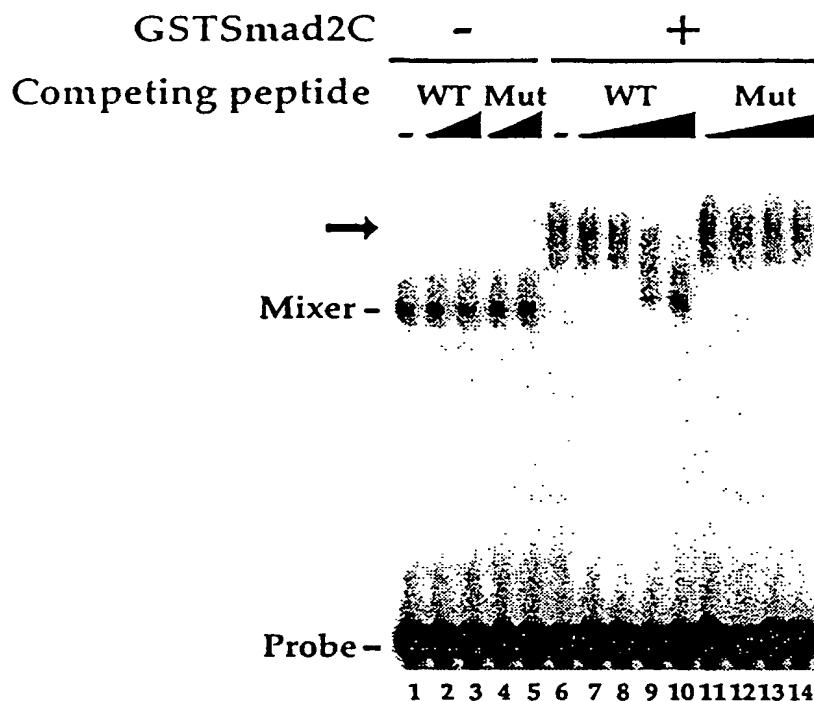
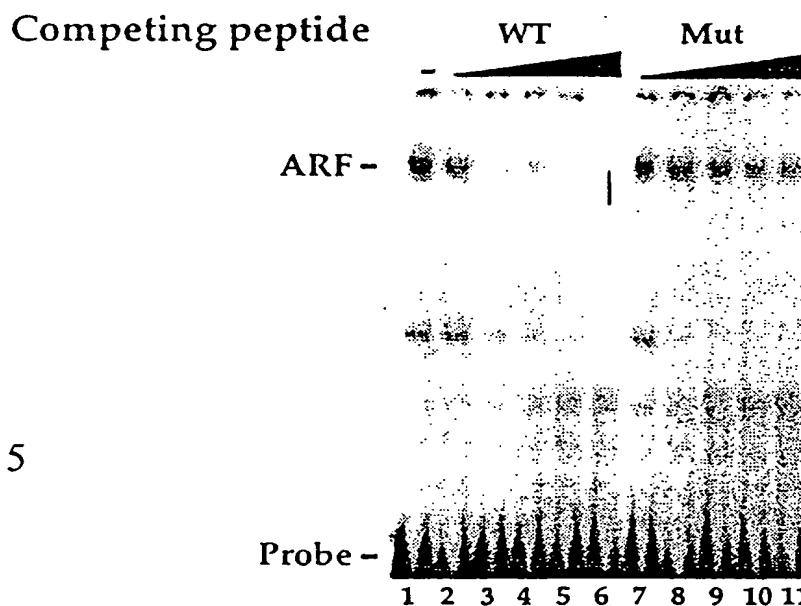
**A**Probe: DE  
Protein: Mixer**B**Probe: ARE  
Protein: Embryo extract

Figure 5

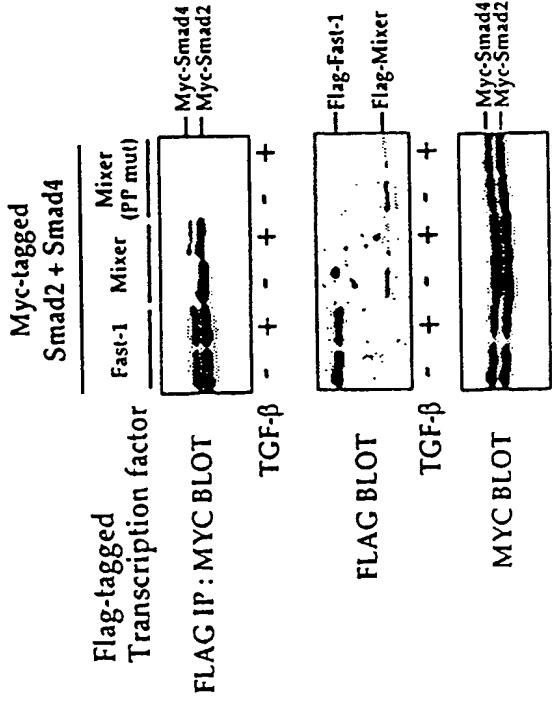
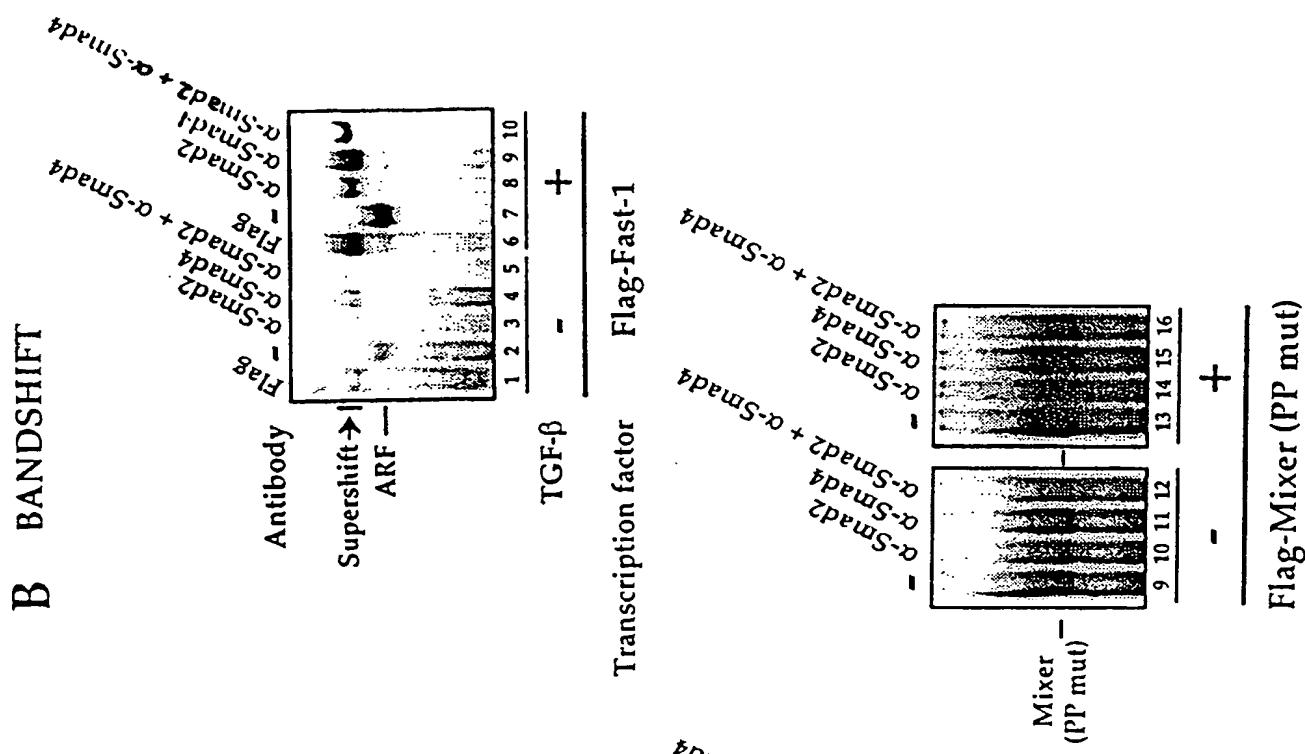
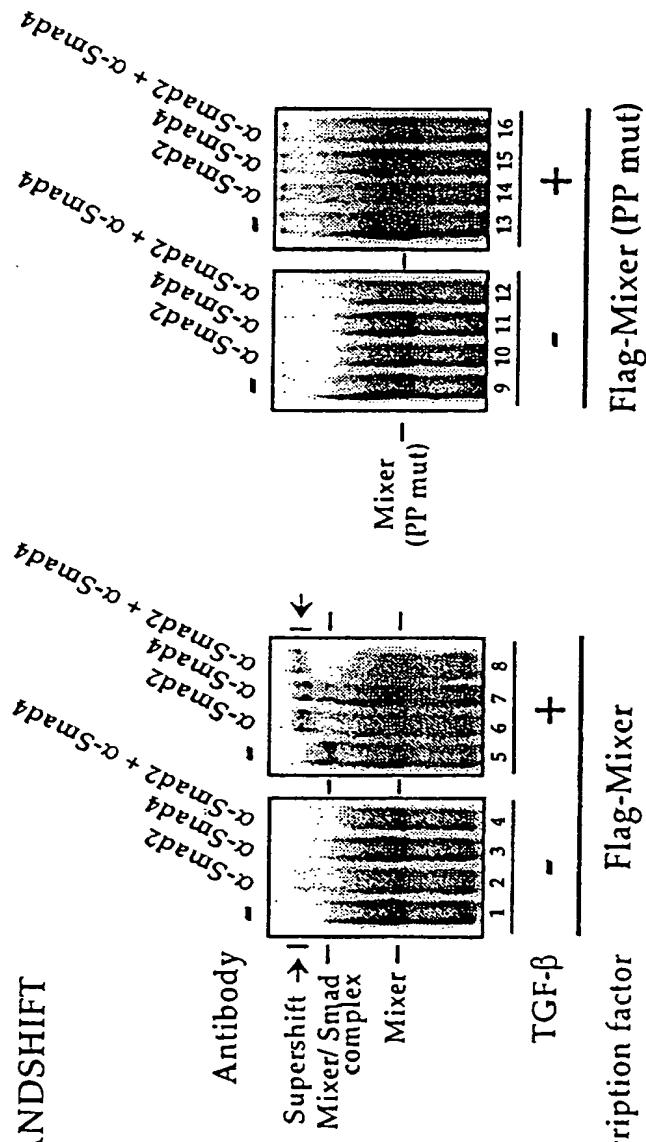
**A CO-IMMUNOPRECIPITATION****B BANDSHIFT****C BANDSHIFT**

Figure 6

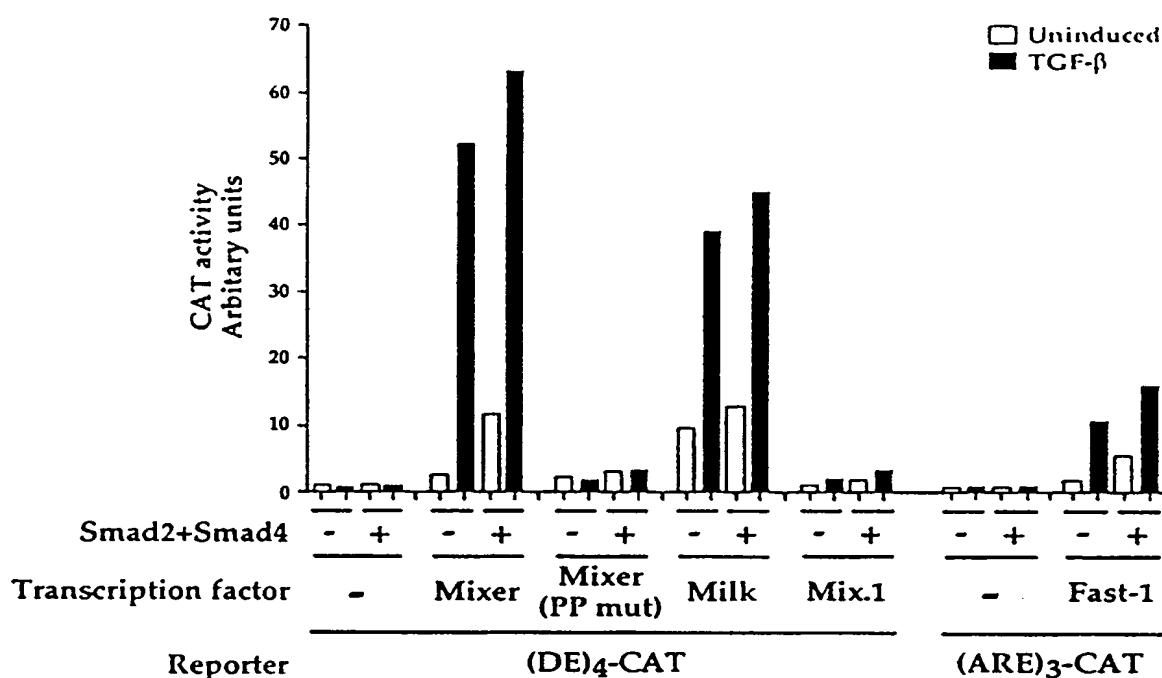
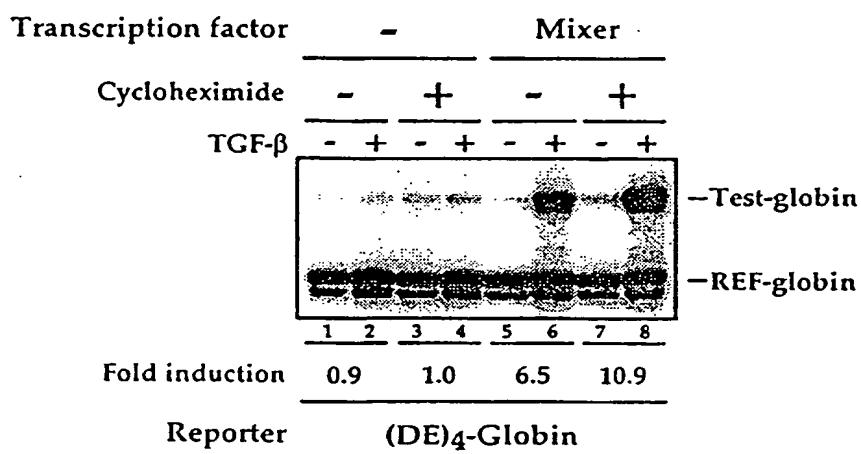
**A****B**

Figure 7

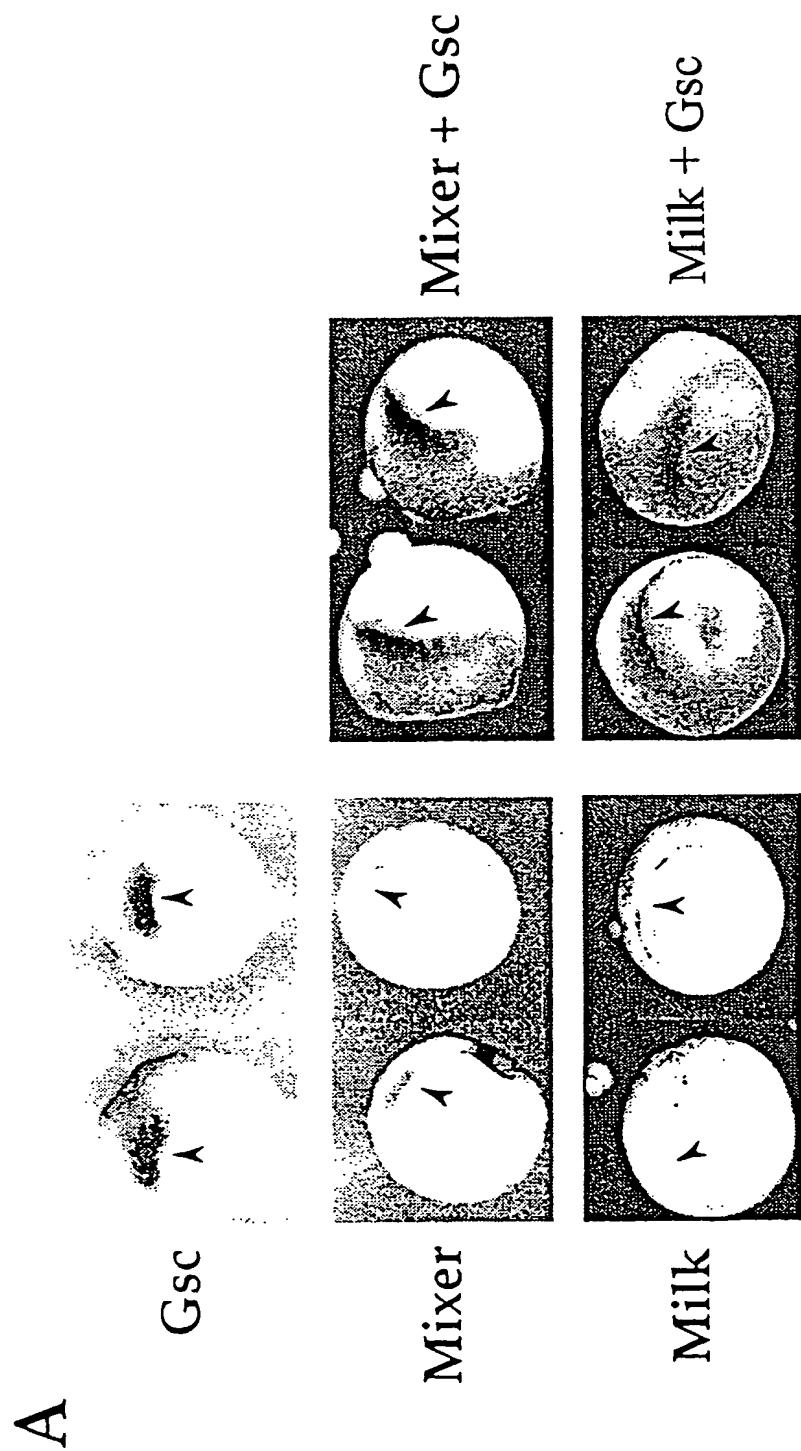


Figure 8

B

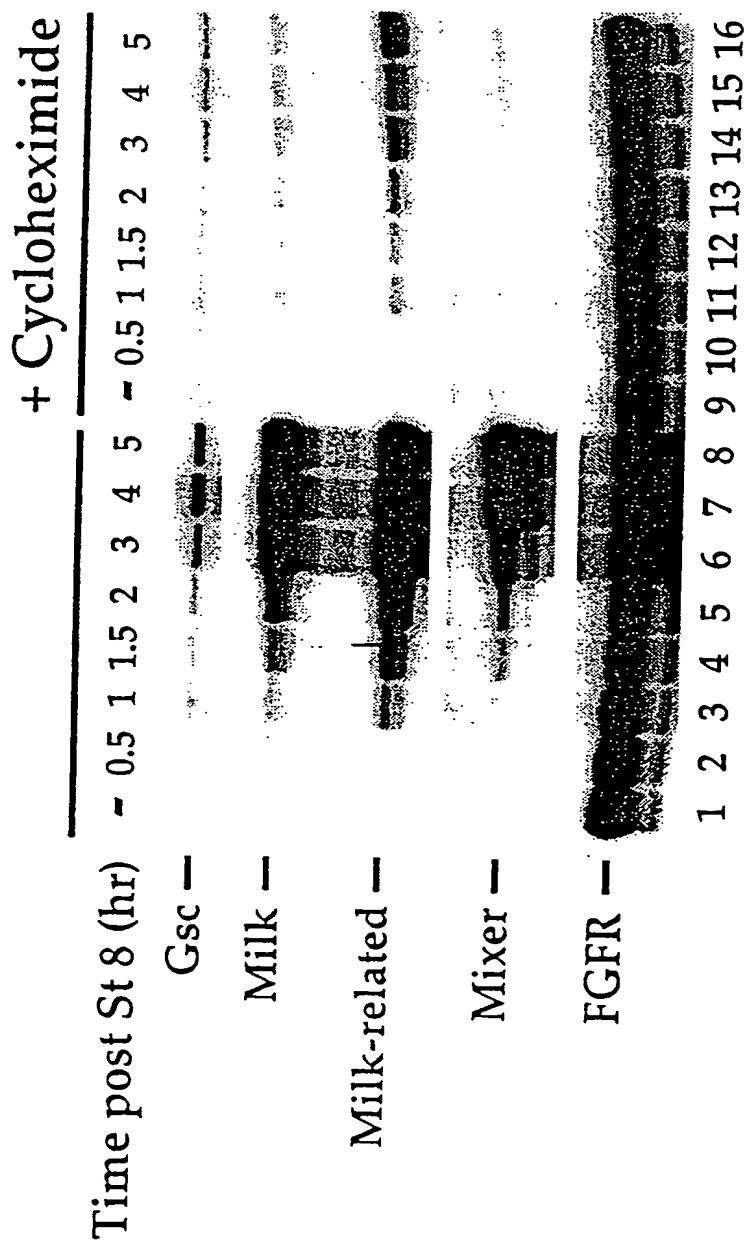


Figure 8

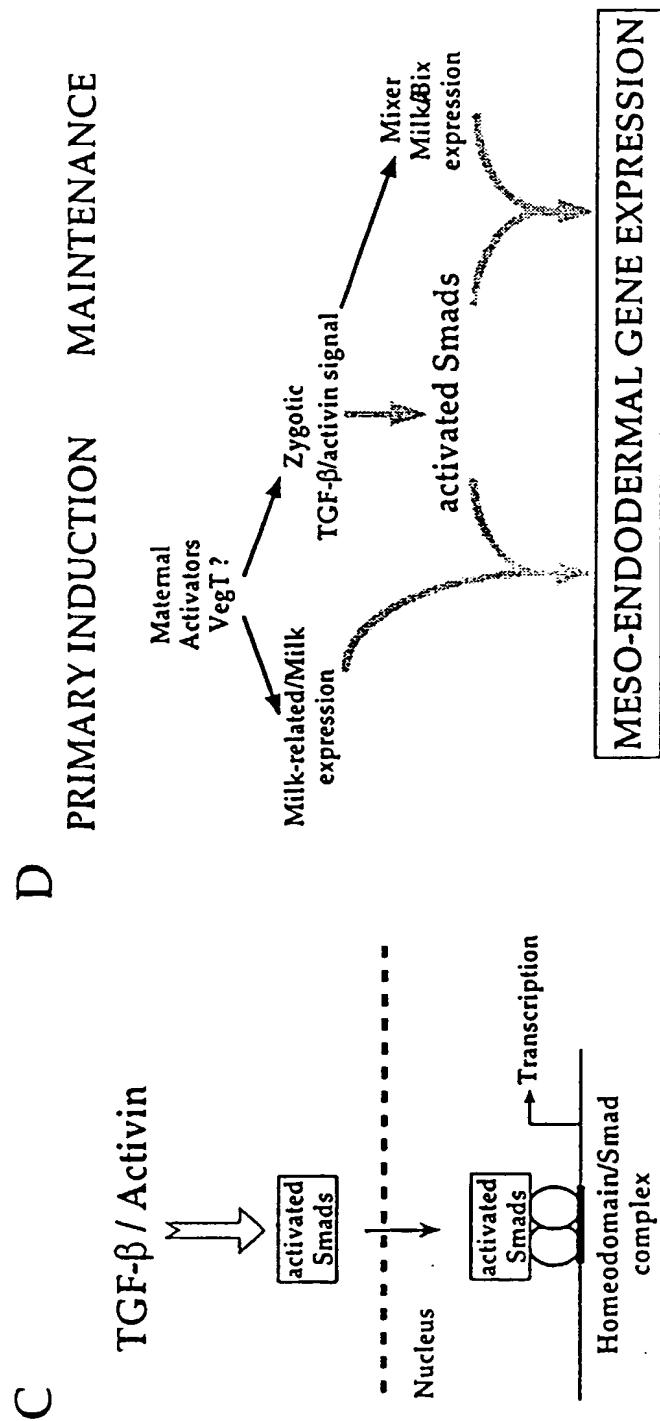


Figure 8

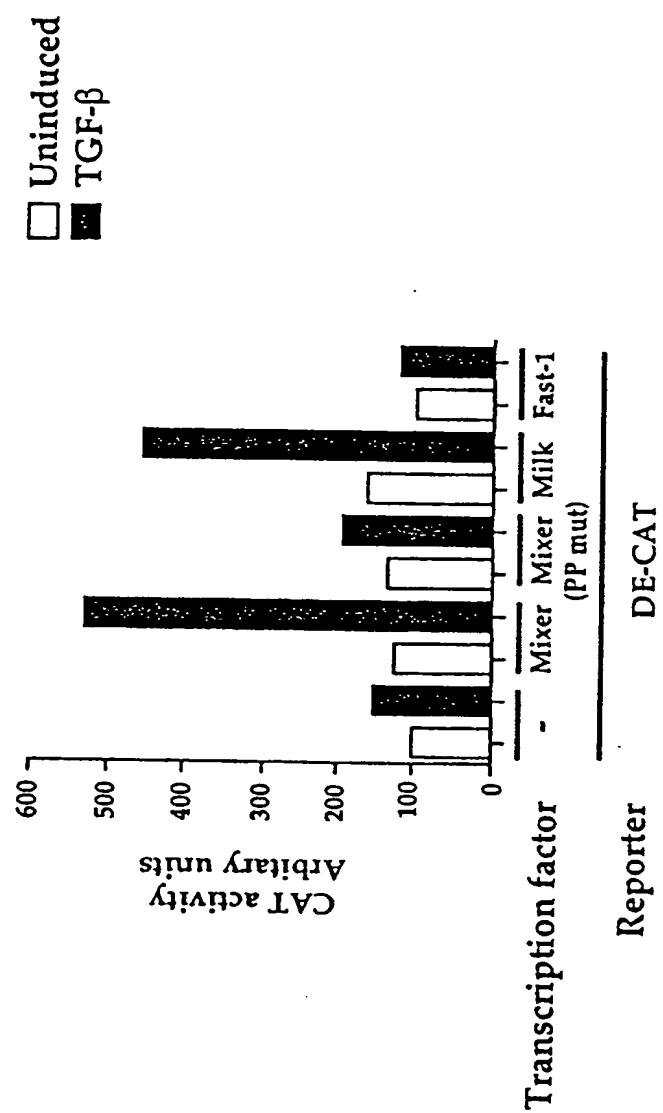
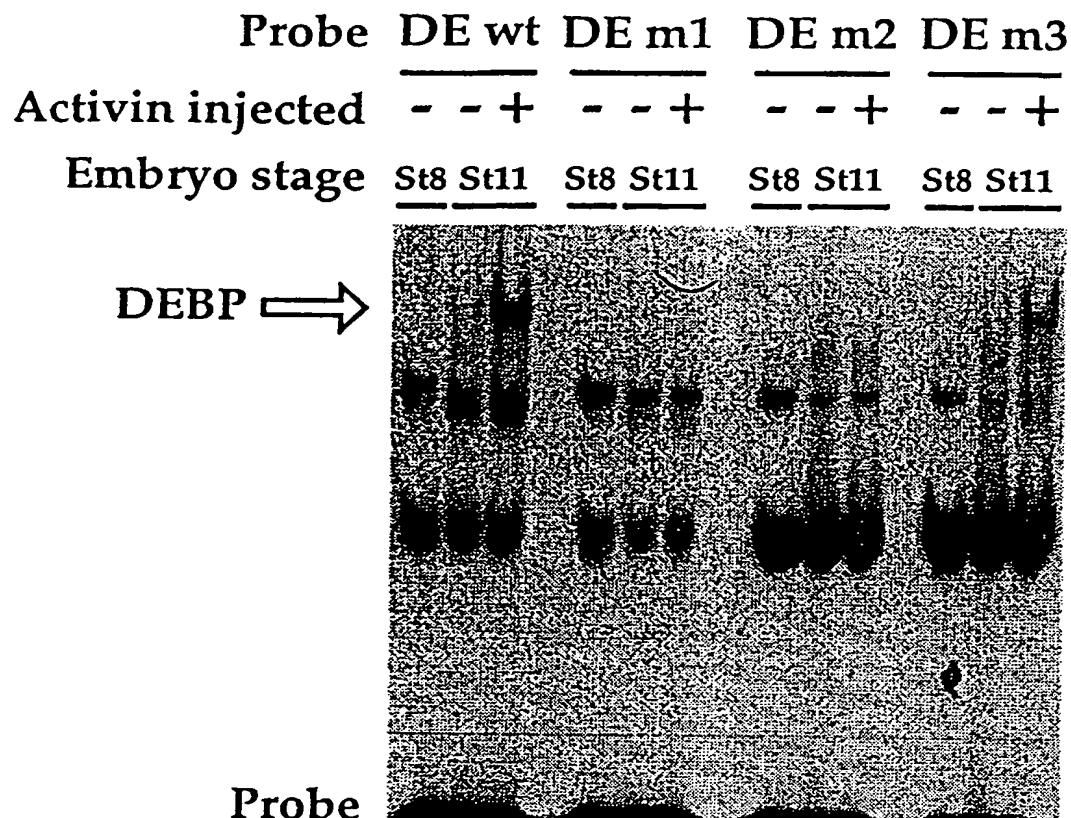


Figure 9



DE wt      → ← ←  
               CATTAATCAGATTACCGGTGAGCAATTAG  
               |  
               -----

DE m1      --G-C-G---C-G-C-----

DE m2      --G-C-----G-C-----G-C-

DE m3      -----TTGT-----G---

Figure 10

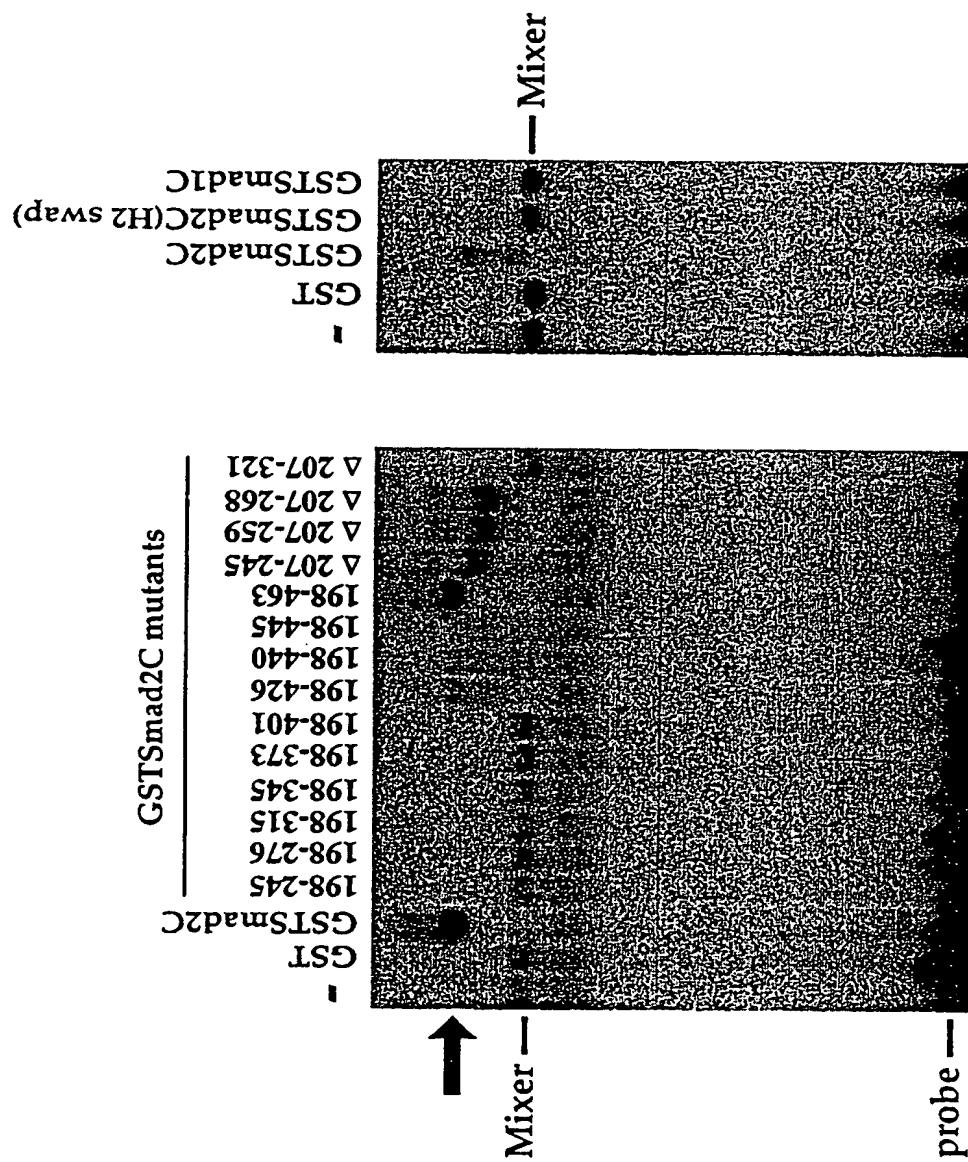


Figure 11

XSmad2

MAGSMSSILPFTPPVVKRLLGWKKSAASGTIGAGGDEQNGQEEKWCEKAVK  
 SLVKKKTGTQLDELEKAITTQNCNTKCVTIPSTCSEIWGLSTANTIDQW  
 DTTGLYSFSEQTRSLLDGRIVYCRLLWRWPDLHSHHELKAI  
 ENCEYAFNLKKDEVCVNPYHYQRVETPVLPVPRHTEILTELPLDDY  
 THSIPENTNFPAIEPQSNYIPETPPPGYISEDGTSQQQLNQSMDTGSP  
 AELSPSTLSPVNHNLDLQPVTYSEPAFWCSIAYYELNQRVGETFHASQPS  
 LTVDGFTDPSNSERFCIGLLSNVNRNAVEMTRRHIGRGRVRLYYIGGEVF  
 AECLSDSAIFVQSPNQCNQRYGWHPATVCKIPPGCNLKIFNNQFAALLAQ  
 SVNQGFEAVYQLTRMCITRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPL  
 QWLKVLTQMGSPSVRCSSMS

Hsmad2

MSSILPFTPPVVKRLLGWKKSAAGSGGGGEQNGQEEKWCEKAVKSLVK  
 KLKKKTGRIDLELEKAITTQNCNTKCVTIPSTCSEIWGLSTPNTIDQWDTG  
 LYSFSEQTRSLLDGRIVYCRLLWRWPDLHSHHELKAIENICE  
 YAFNLKKDEVCVNPYHYQRVETPVLPVPRHTEILTELPLDDYTHSI  
 PENTNFPAIEPQSNYIPETPPPGYISEDGTSQQQLNQSMDTGSPAELS  
 PTTLSPVNHSSLQPVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTV  
 GFTDPSNSERFCIGLLSNVNRNAVEMTRRHIGRGRVRLYYIGGEVF  
 SDSAIFVQSPNQCNQRYGWHPATVCKIPPGCNLKIFNNQFAALLAQSVNQ  
 GFEAVYQLTRMCITRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPLQWLD  
 KVLTQMGSPSVRCSSMS

Figure 12

Xsmad3

MSSILPFTPPIVKRILLGWKKGEQNGQEEKWCEIKAVKSLVKKKSGOLDE  
 LEKALTQSISTKCITIPRSLDGRLQVSHRKGLPHVIIYCRLLWRWPDLHSH  
 HELRAMEVCEYAFSMKKDEVCVNPYHYQRVETPVLPPLVPRNTEIPAEF  
 PSLDDYSHSI PENTNF PAGEI EPQINYI PET PPPGYLSEDGETSDQMNHSI  
 DTGSPNLS PNSMSPAHSNM D LQPVTYCEPAFWCSISYYELNQRVGETFHA  
 SQPSMTVDGFTDPSNSERFCI GLLS VNRNA AVELTRRHIGRGVRILYYIG  
 GEVFAECLSDNA IFVQSPNCNQRYGWHPATVCKI PPGCNLKIFNNQEEFAA  
 LLAQSVNQGF EAVYQLTRMCTIRMSF VKGWGA EYRRQTVTSTPCWIELHL  
 GPLQWLDKVLTQMGSPSIRCSSVS

Hsmad3

MSSILPFTPPIVKRILLGWKKGEQNGQEEKWCEIKAVKSLVKKKSGOLDE  
 LEKAITTQNNTKCITIPRSLDGRLQVSHRKGLPHVIIYCPVRRWPDLHSH  
 ELRAMELCEFAENMKKDEVCVNPYHYQRVETPVLPPLVPRHTEIPAEFP  
 PLDDYSHSI PENTNF PAGEI EPQSNI PET PPPGYLSEDGETSDQMNHSMD  
 AGSPNLS PNPMSPAHN NLDLQPVTYCEPAFWCSISYYELNQRVGETFHAS  
 QPSMTVDGFTDPSNSERFCI GLLS VNRNA AVELTRRHIGRGVRILYYIG  
 EVFAECLSDSAIFVQSPNCNQRYGWHPATVCKI PPGCNLKIFNNQEEFAA  
 LLAQSVNQGF EAVYQLTRMCTIRMSF VKGWGA EYRRQTVTSTPCWIELHLN  
 GPLQWLDKVLTQMGSPSIRCSSVS

Figure 12

301/1		331/11	361/21
ATG TCC TCG ATA CTT CCC TTC ACT CCC CCC ATT GTC AAC AGG CTG CGA TGG AAG AAC CGA GAG CAG AAC CGA			
M S I L P F T P P I V K R L L G W K K G E Q N G			
391/31		421/41	451/51
TGC GAG AAG GCA GTG AAA AGT CTG CTG AAG AAG CTG AAC AGC GGC CAG CTC GAC GAG CTG GAG AAG GCA CTG			
C E K A V K S L V K K L K S G Q L D E L E K A L			
481/61		511/71	541/81
ACC ACC AAG TGC ATC ACC ATC CCC AGG TCT CTG GAT CGG AGA CTC CAG GTG TCC CAT CGT AAG GGG TTG CCT CAT			
S T K C I T I P R S L D G R L Q V S H R K G L P H			
571/91		601/101	631/111
CTC TCG AGG TCG CCA GAT CTG CAC AGT CAC CAC CAC GAG CTT CGA CCC ATG GAG GTG TGT GAA TAT GCC TTC AGC ATG			
L W R W P D L H S H E L R A M E V C E Y A F S M			
661/121		691/131	721/141
TGT GTG AAT CCT TAT CAC TAC CAG AGA GTG GAG ACT CCA GTT CTA CCT CCT GTG CTG GAT CCA CGA AAC ACC GAA			
C V N P Y H Y Q R V E T P V L P P V L V P R N T E			
751/151		781/161	811/171
CCT TCA CTT GAT GAT TAC AGC CAT TCC ATT CCG GAA AAT ACC AAT TTC CCA GCA CGC ATC GAG CCA CAG AAC AAC			
P S L D D Y S H S I P E N T N F P A G I E P Q I N			
841/181		871/191	901/201
CCT CCT CCC GGT TAC TTG AGC GAA ACA AGC GAC CAA ATG AAT CAC AGT ATA GAT ACA GCA CGC TCT CCA			
P P G Y L S E D G E T S D Q M N H S I D T G S P			
931/211		961/221	991/231
TCT ATG TCT CCT GCT CAT AGC AAC ATG GAC CTG CAG CCT GTC ACA TAC TGC GAG CGC CCC TTT TGG TGT TCC ATC			
S M S P A H S N M D L Q P V T Y C E P A F W C S I			
1021/241		1051/251	1081/261
ANC CAA CGC GTA CGG GAG ACC TTC CAC CCT TCC CCC TCC ATG ACA GTG GAT GGA TTC ACC GAT CCT TCC AAC			
N Q R V G E T F H A S Q P S M T V D G F T D P S N			
			TCT GAA CGT TTC TGC S E R F C

1111/271 CTG CGC TCG TTG TCC AAC GTA AAT CGG AAT GCA GCT GTG GAG CTG ACA CGG AGA CAC ATC GGG AGA GGC GTG CGG CTC L G L S N V N R N A A V E L T R R H I G R G V R L	1141/281 1171/291 TAT TAC ATT GGA
1201/301 GGG GAA GTG TTT GCC GAG TGC CTC AGT GAC AAT GCC ATA TTT GTA CAG TCC CCA AAT TGT AAC CAG CGC TAC GGT TGG Q E V F A E C L S D N A I F V Q S P N C N Q R Y G W	1231/311 1261/321 Y I G
1291/331 GTC TGC AAC ATT CCA CCA CGC TGT AAC CGT CTG AAG ATA TTT ATT AAC CGG GAG TTT GCT GCT CTT TTT CCT CAG TCA GTC V C K I P P G C N L K I F N N Q E F A A L L A Q S V	1321/341 1351/351 H P A T
1381/361 GAG GCT GTG TAT CAG CTT ACG AGG ATG TGC ACC ATA CGC ATG AGT TTC GTC AAA CGG TGG CGA GCC GAA TAC AGG CGA E A V Y Q L T R M C T I R M S F V K G W G A E Y R R	1411/371 1441/381 N Q G F
1471/391 AGC ACC CCC TGC TGG ATC GAG CTG CAC TTG AAC CGG CCC TTG CAA TGG TTG GAT AAG GTT CTC ACT CAG ATG GGG TCT S T P C W I E L H L N G P L Q W L D K V L T Q M G S	1501/401 1531/411 T V T
1561/421 TGC TCC AGT GTT TCT TAA C S S V S *	CCA AGT ATC CGC P S I R

Figure 12

**A**

Mixer	KH-SQMPFHP <u>SLLMDENNFPPNKTITPD</u> MNV--RIPPIPVSA <u>PSNNHS</u>
ZF Mixer	ANHA <u>KSTMKQFLV-EYDNFPPNKTIGPEMKV--VIPPPLPSQS</u> NFM <u>SS</u>
Milk	RH-NQVSMHSN <u>LMMDF---PPNKTITPD</u> MNT--IIPQITDATGWSSQE
Bix3	RQ-NQVTMHSN <u>LVMEF---PPNKTITPD</u> MNT--IIPQIPGATGWKNQE
XFast1	DSPRG <u>PQSPLIDLDNMILRAMPPNKS</u> V-FDVL <u>T--SHPGDLVHPSFLSQ</u> C
HFast1	ETRGPP <u>GLLCQLDALFQGVPPNKS</u> I-YDVWV--SHPRDLAA <u>PAPGW</u> LL
MFast2	ESQGSQ <u>DLICLDDSLFQGVPPNKS</u> I-YDVWV--SHPRDLAA <u>PAPGW</u> LL
XFast3	PQIPLTPK <u>PPELKNA</u> PSDFPPNKT <u>V-FDIPVYTGHPGFLASQSLFSPH</u>

Figure 13

**B**

Mixer	Mixer SIM peptide
ZF Mixer	SQMPFHPSLLMDFFNNFPENNKTITPDMMNVRIPIPPVSAPSNNH-
Milk	AKSTMKQFL-VEYDNFPPNKTTIGPEMKVVVIPPLPSQSNNFMMSS
Bix3	NQVSMHSNLMMDF---PPNKTITPDMMNTIIPQITIDATGWS---
Bix1	NQVSMHSNLMMDISNFPPTKTTANMNTIIPQMPGASCWS---
Bix4	NQVSMHSNIMMDFSNEQPKKTVTPDMNTIIPQIPDATGWS---
Mix. 1	QQMPVQPMMLNSF---QTNKNIKPEVYTTSPQIPVSTTS---
Mix. 2	QQMPAQPMFMNSF---QTNKIIKSMDTTSPPIPVSTTSSHH-

→ ←

SRMNVENTKEAGPLVSLPEDVYEE 371  
 SSPKHIACSVQNMHSVQTQPELFAT 327  
 SQEGTDAYSTQGALPRAQCSPYQQ 400  
 NQEDINTYSTQGALSRAGGSSYGL 382  
 SHEDINAYSTQGAVPMAGCSPYGH 401  
 NQEGTDAYSTQEALPRAQCSPYGH 380  
 SQVSLFANQEPCHMSTTQGGTYQQ 377  
 SQMSLFLAGQDPCHMSTAPGGTYQQ 369

Figure 13

C  
XFast3

MSFGLIHPWDVAFRPSPPHNLLEKKVVPPIGADREKSLPSPKEDSDGAREPDSTVDLRKNNKKKNYQ

RYAKPPSYLAMISLVITQNSPEKRLKLSQLQDISSLFPFFKGNTYQGWKDISTRHNLSSNDCFRKV

LKDPLKPQAKGNWYTVDVTRIPPDALKLQNTAVTRQDLFPLDLAPYILHGQPYRSLERLSANHTR

GRTTPRMEPEVQIPVSDPAVSFPAMILWNLPTSYSKCVAPNVVAPPsiHPLLlySNFSPSISIYNYL

PPPYGSPVYSDRRDLLASGLHPQIPLTPKPPPELKNAAPSDFPPNKTVFIDIPVYTGHPGFLASQSLF

SPHLPTATPPLVGYRPSGL

Figure 13

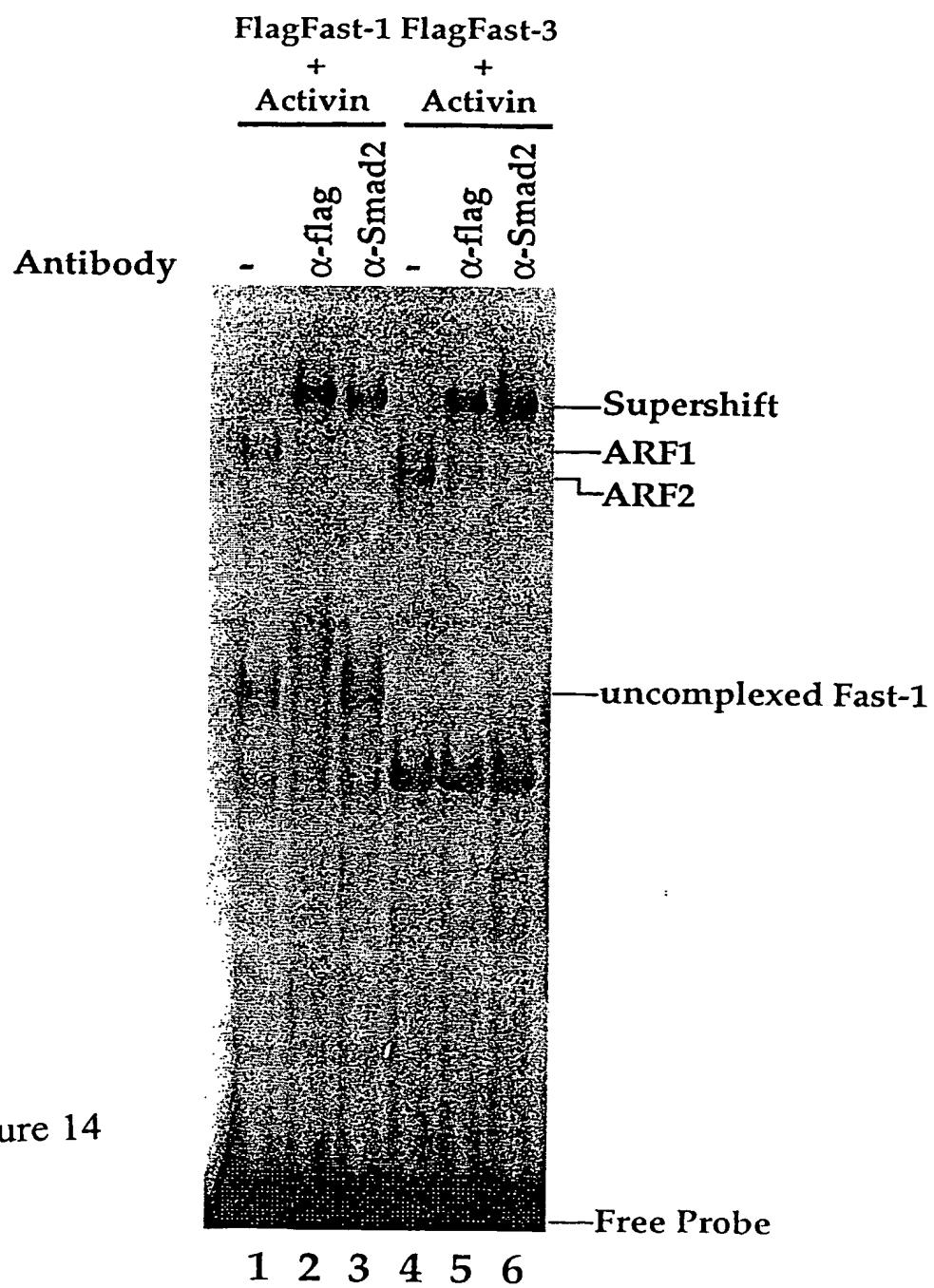


Figure 14

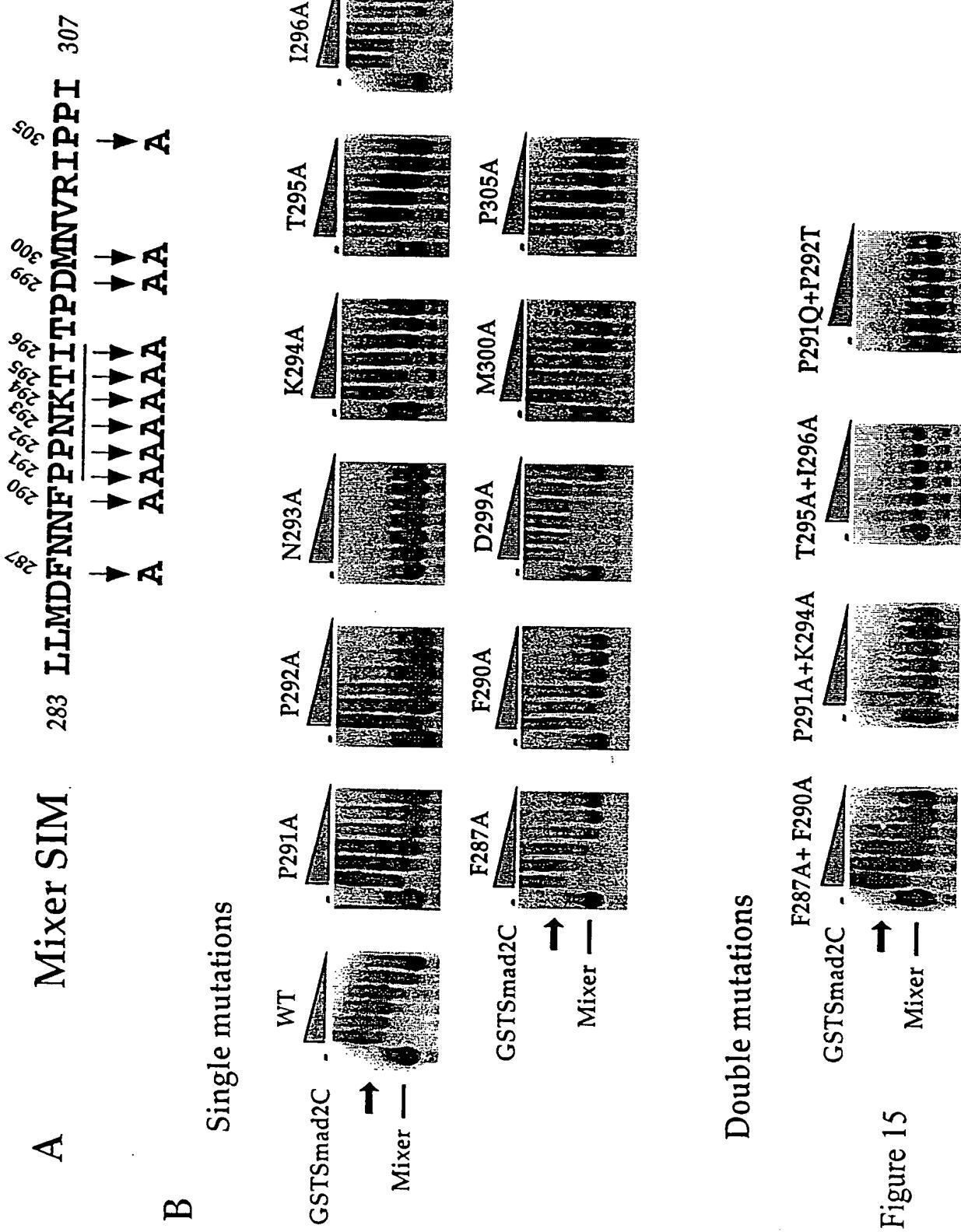
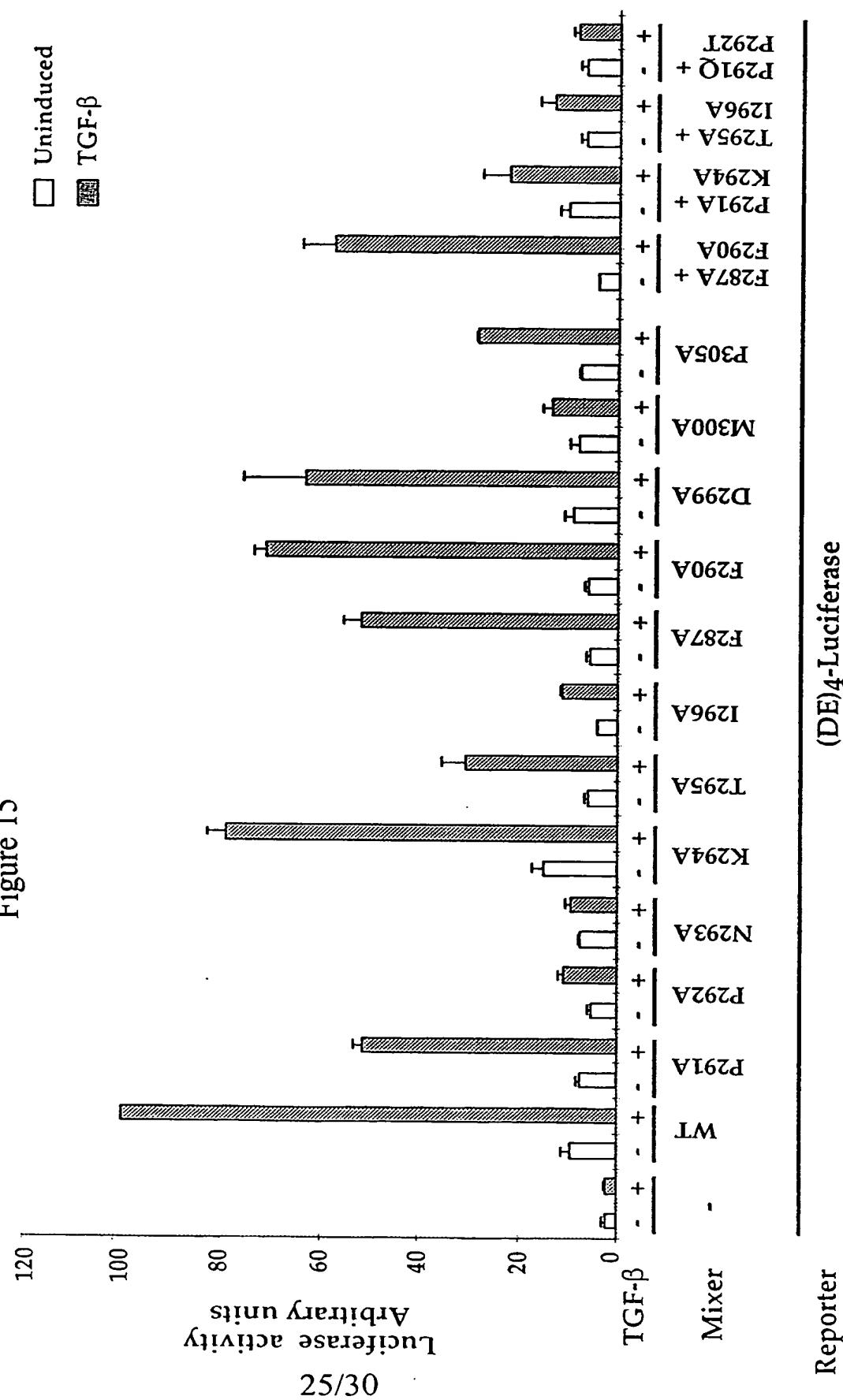


Figure 15

C

Figure 15



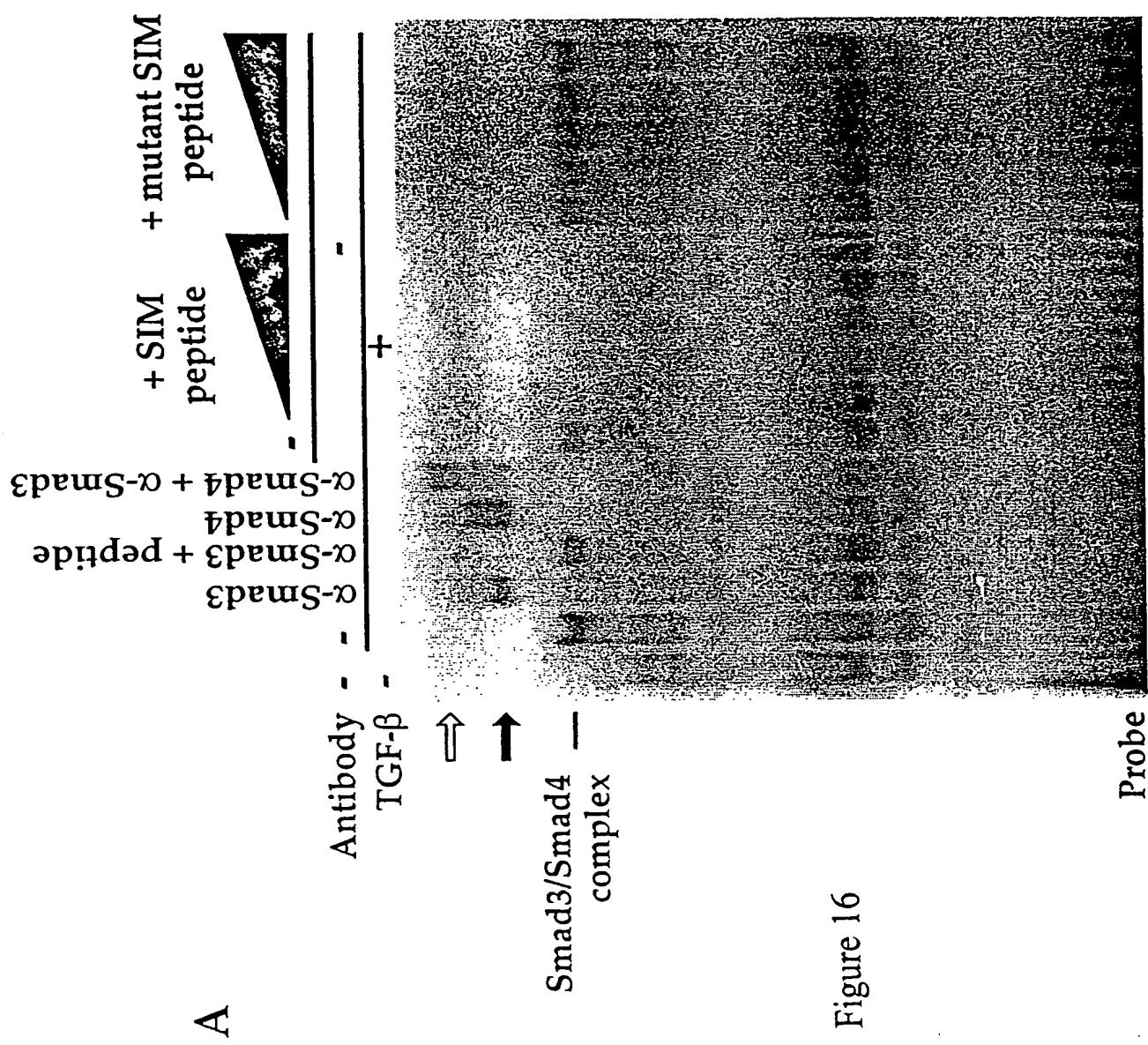


Figure 16

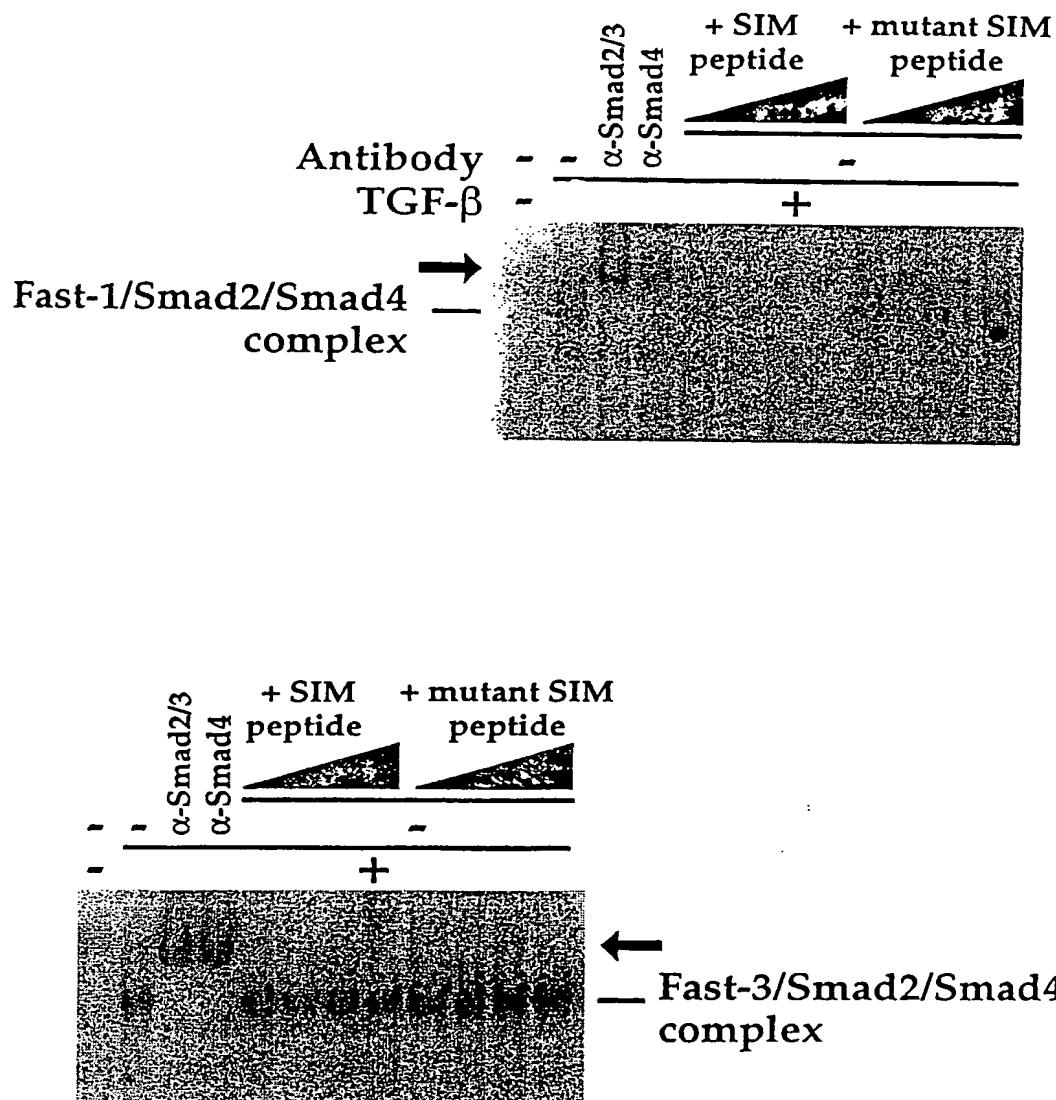
**B**

Figure 16

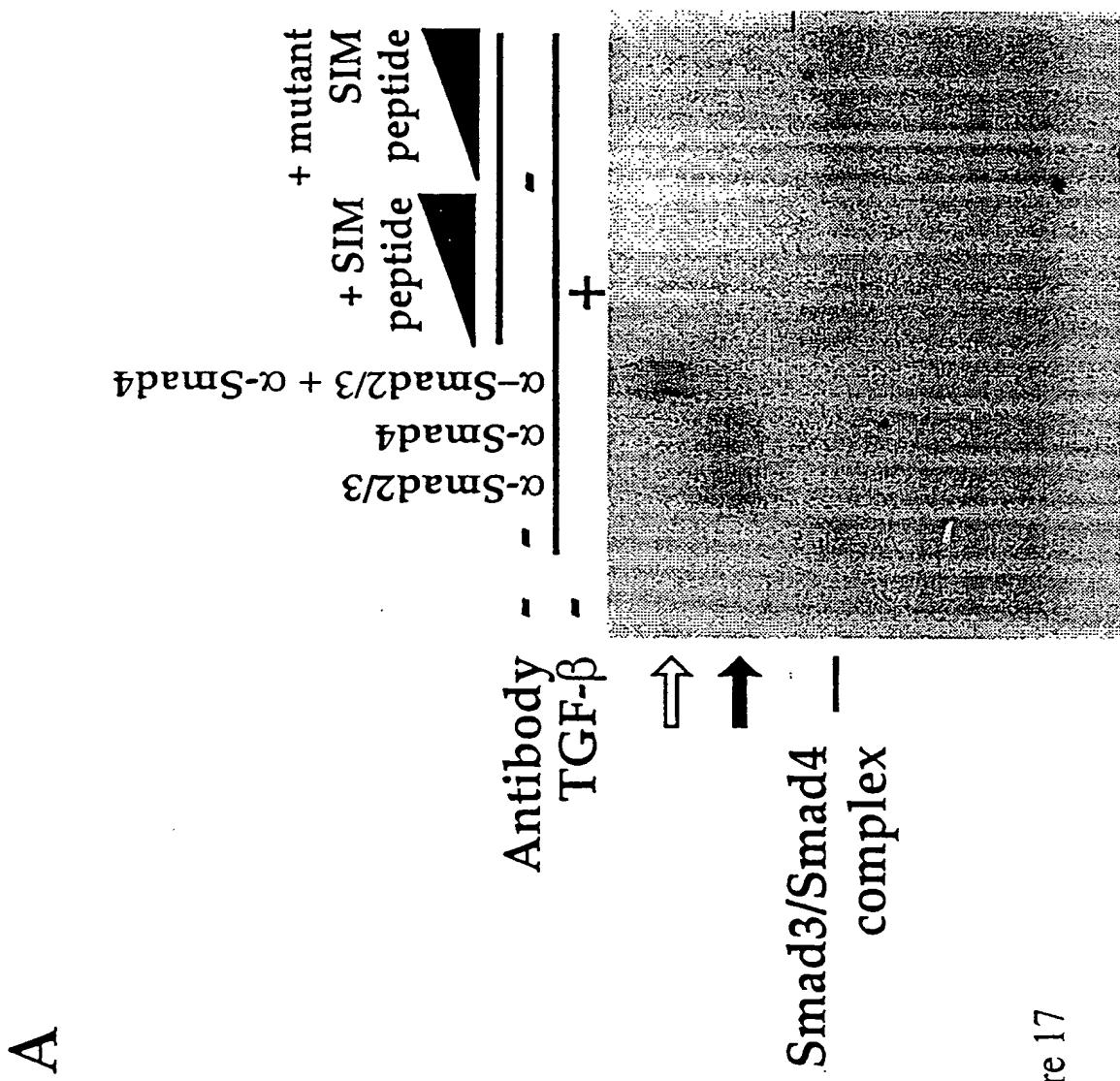


Figure 17

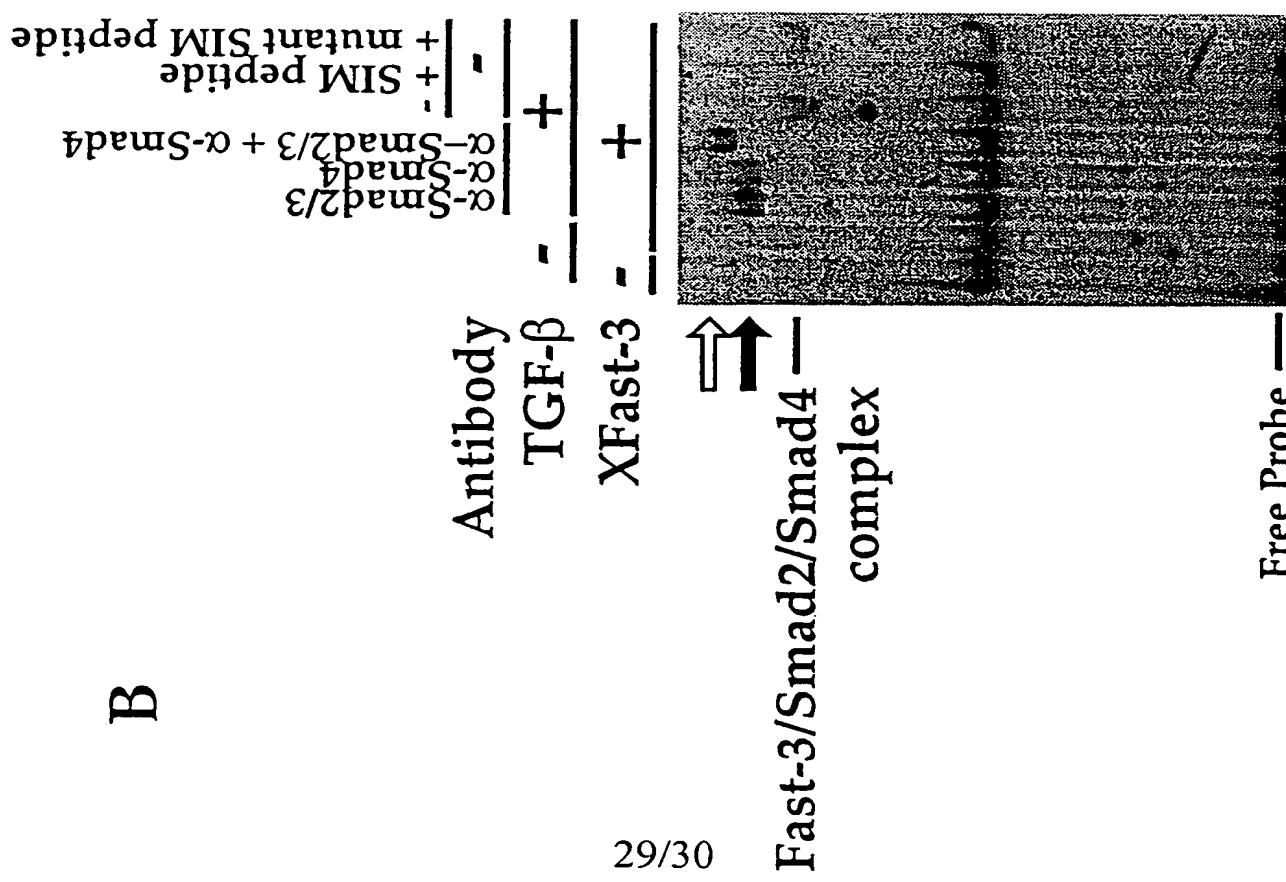
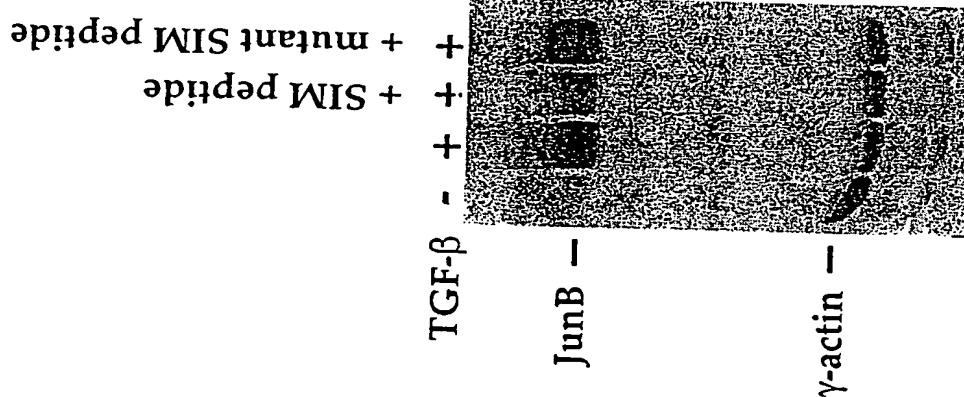
**C**

Figure 17

Figure 18

1 ATGTCTTTG GGCTTCACCC ATGGGATGTG GCCTTCAGAC CTTCACCCCC  
           TCACAACCTG GAGAAGAAAG TCGTCCCCC AGGGGCCGAC AGAGAGAAAGT

101 CGCTTCCTTC CCCAAGGAG GACAGTGATG GGGCCGGGA GCCCGACTCC  
       ACTGTGGATT TGAGGAAGAA GAACAGAAC AACAGAACT ACCAGAGATA

201 CGCCAAGCCC CCCTATTCTT ACCTGGCCAT GATCTCCCTG GTCATCCAGA  
       ACTCCCCCGA GAAGAGGGCTC AAACTCTCCC AGATCCTGCA GGACATCAGC

301 TCTCTGTTTC CATTCTCAA GGGCAACTAC CAGGGCTGGA AGGATTCCAT  
       TCGGCATATAAT TTGTCTTCCA ACGACTGTGTT CAGAAAGGTT CTGAAGGATC

401 CGCTCAAGGCC ACAGGCCAAG GCGAATTACT GGACAGTAGA CGTGACCCGG  
       ATCCCCCAG ACGCTTTGAA GCTCCAGAAC ACGGCGGTGA CCCGGCAGGA

501 CCTGTCCCC CTGGACCTGG CCCCTACAT CCTACATGGG CAGCCGGTACA  
       GGAGTCTGGA GAGGCTCTCG GCCAATCACA CGAGGGGGCG CACGACCCCC

601 AGGATGGAGC CTGAAGTTCA GATTCCAGTG TCAGACCCAG CTGTCAGTT  
       CCCCATGATC CTATGGAATC TGCCGACATC CTACAGCAA TGTGTGGCCC

701 CCAAATGTAATG GGCCTCTCCC AGCATTCAAC CCCTCTTGTG GTACTCAAAC  
       TTCCCTTCCA TTTCATTTA TAATCTACCTG CCCCCCCCT ATGGCAGCCC

801 CGTGTACTCA GACAGACGAG ATCTTCTTGC CTCCGGCTG CACCCCCAAA  
       TCCCTCTCAC CCCAAACCC CCAGGGCTGA AGAACGGCCC CAGGGACTTC

901 CCCCCAAACA AGACAGTGT TGACATCCCC GTCTATACTG GCCACCCGGG  
       GTTCCCTGCT AGCCAAAGCT TGTTCAGGCC ACACTTGCC ACGGGCTACAC

1001 CCCCCCTCGT GGGCTACCGG CCATCTGGGC TATGA

30/30